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16

**RAW SEQUENCE LISTING**

DATE: 12/19/2003

PATENT APPLICATION: US/09/680,121C

TIME: 16:00:51

Input Set : A:\Amended Sequence Listing for 107-206-C-D.txt

Output Set: N:\CRF4\12192003\I680121C.raw

3 <110> APPLICANT: FRENCH, Cynthia K.  
 4 YAMAMOTO, Karen K.  
 5 EL SHAMI, A. Said  
 7 <120> TITLE OF INVENTION: Prostate Cancer-Specific Marker  
 9 <130> FILE REFERENCE: 107-206-C-D  
 11 <140> CURRENT APPLICATION NUMBER: 09/680,121C  
 12 <141> CURRENT FILING DATE: 2000-10-04  
 14 <150> PRIOR APPLICATION NUMBER: 60/041,246  
 15 <151> PRIOR FILING DATE: 1997-03-07  
 17 <150> PRIOR APPLICATION NUMBER: 60/047,811  
 18 <151> PRIOR FILING DATE: 1997-05-15  
 20 <150> PRIOR APPLICATION NUMBER: 09/036,315  
 21 <151> PRIOR FILING DATE: 1998-03-06  
 23 <150> PRIOR APPLICATION NUMBER: 09/535,597  
 24 <151> PRIOR FILING DATE: 2000-03-27  
 26 <150> PRIOR APPLICATION NUMBER: 09/680,121  
 27 <151> PRIOR FILING DATE: 2000-10-04  
 29 <160> NUMBER OF SEQ ID NOS: 27  
 31 <170> SOFTWARE: PatentIn Ver. 2.1  
 33 <210> SEQ ID NO: 1  
 34 <211> LENGTH: 3891  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Homo sapiens  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: CDS  
 40 <222> LOCATION: (151)..(1425)  
 42 <220> FEATURE:  
 43 <223> OTHER INFORMATION: product = Repro-PC-1.0  
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 48 cgttccgaaa gccggcgctt gagatccagg caagtgaatc cagccaggca gttttccctt 120  
 50 cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174  
 51 Met Ala Pro Ile Thr Thr Ser Arg  
 52 1 5  
 54 gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 222  
 55 Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe  
 56 10 15 20  
 58 ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga 270  
 59 Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg  
 60 25 30 35 40  
 62 aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 318  
 63 Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val  
 64 45 50 55

p.6  
**ENTERED**

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66 ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag 366
67 Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
68          60          65          70
70 ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca 414
71 Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
72          75          80          85
74 aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat 462
75 Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
76          90          95          100
78 ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat 510
79 Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn
80 105          110          115          120
82 gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct 558
83 Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro
84          125          130          135
86 gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag 606
87 Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu
88          140          145          150
90 aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa 654
91 Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys
92          155          160          165
94 gca ttt gtg gtc aat atc aag gaa gcc cgt ggc ttg cca gcc atg gat 702
95 Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp
96          170          175          180
98 gag cag tcg atg acc tct gac cca tat atc aaa atg acg atc ctc cca 750
99 Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro
100 185          190          195          200
102 gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat 798
103 Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp
104          205          210          215
106 cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa 846
107 Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln
108          220          225          230
110 atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt 894
111 Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe
112          235          240          245
114 tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att 942
115 Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile
116          250          255          260
118 gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga 990
119 Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg
120 265          270          275          280
122 aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc 1038
123 Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys
124          285          290          295
126 tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga 1086
127 Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg
128          300          305          310
130 cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa 1134

```

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```

131 His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys
132          315          320          325
134 gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat 1182
135 Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His
136      330          335          340
138 gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt 1230
139 Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
140 345          350          355          360
142 gat att cct tgt gag ggc ctt gaa gat ata agt gtt gaa ttt ttg gtt 1278
143 Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val
144          365          370          375
146 ttg gat tct gaa agg ggg tcc cga aat gag gta atc ggg cag tta gtc 1326
147 Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val
148          380          385          390
150 ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc 1374
151 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
152          395          400          405
154 tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat 1422
155 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
156      410          415          420
158 ggt tagcatccta gccgtgagtt ggaacttaaa gggttttact aggcaaggag 1475
159 Gly
160 425
162 aaatttttctt tcttttctata ttggattgca agcttgggaa atcaagctac ctttttgttg 1535
164 ttgttgttgt tgctagaaat ggattgaatt agtagaccag aaagtaactt caaatgtgta 1595
166 ttatgataat ttccctattt attagaagag ttggataaat tttcataaga tattcaatat 1655
168 ctccctcaga ttaccagtga tataactagg aatagtcaga cattttatga atactgtgcc 1715
170 agaatcccaa attataaatg tgacaatctc attggaacat gtcacaaaaa gttaatgtga 1775
172 ttaagattta aaaacgaaaa gtatgccttg ccttgtgaaa atttatccat ttatcttcag 1835
174 gttgggggaa atcaattttt ctttaatcca aagatactaa aaaaatgtcc tccagtttgt 1895
176 atttattaat tctgtcatgt gcaaatggtt gtcctgcata taaaagtatc tggtcatttc 1955
178 agtttggttt gtaattattt gatgcaattt tatcataaga gtaactcaga ttcatttcaa 2015
180 aaggacagtg aacaagctga gaaattattt tatcaaaggg ctgagttgag aacactgtgg 2075
182 ctgaaatata atttttctcc cccctaagggt tacatgtgag tcaaaatttt gtaaaatata 2135
184 acctcacata agaaccatgg ccttggatta ttcactgcct gtcacaagcc tcagtgtggc 2195
186 ctgagaaatc cctatgtacc tttgtgaaat tggtgaatta gttagtgaat aaagaaataa 2255
188 acttcaacta gaaatccagt tagaagtgca attttcttat aggaaatagg tatagtgtgc 2315
190 aagtgtactt ttaaggccat cgtttgtacc cagagtcggc atggccacct aagtcttcat 2375
192 ttaatttatt gtcccccaga aaagattaag atgctacttg aaaagactgt gaagattttt 2435
194 tacattgcc aataaaaagt gttacttaac caacaaacaa atgtaagact acaaaatcgt 2495
196 tcaagagcaa ttctaataata atttacatat gttcacgcaa aatatgctta ggctgtcaaa 2555
198 ttagcacaa aaagaatgtg ttctactatc ttttctaggc taatttgtct tgagctgttg 2615
200 tctatagagc agtttacaga cttgtgtcct gtatcatttt ccagtgccag ggttctgaaa 2675
202 ttcattcaga acctgttaga ttaaagctgc accctgtgat tatttgaaaa gaattagctt 2735
204 gagagtaatg tcactatatt tgagttctta gagaagtatg agtggaactt gagtacagtt 2795
206 gaattattaa atatgcaagt tagaaattaa gtctactgaa aaatttacat tttgagtcag 2855
208 gttttgtgtc agtactttag cagtttttga gaatgtgttt gatatcacag tgtttgtaaa 2915
210 ttctatgaaa aatgcatttt ccaacaact tatacatgct ttttatgact atgcctaata 2975
212 taaagaaaat gtattacatt ctgtatgtac aaagattaaa aatcaacctc ttttttgtgc 3035

```

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214 tttaaaatga ctttgggatt aaaaaagcat atttcccaat cattgtcttc attccactac 3095
216 aaagtcacct cacagcatct tgctccactc ggcattctctg tgaaagcaac atgaaatgaa 3155
218 ctgtagtagg tgtgtagttt ggggaagtca aatggccatt ttatgtatgt gcatttggta 3215
220 tcatgggccg tggaacagaa tataatgttg acctctgaaa agttgtaagg ggccaaatct 3275
222 aagtattctt cacggcagcc agaagttaat ggtggttagca gctgaggat ggttgttggg 3335
224 cgaggccgat tttttttttt taacatggaa caatgaaacc aacaacaaac atttttaaaa 3395
226 ttaaaatgga taatttgtaa atagttttta gcttttaaaa tttaaagtgt ttttgagtgt 3455
228 gaaaagttga gtaaaactat ttgcaactgg ttttcagaaa agagaaaaga aacaacaaag 3515
230 gaattgaaac aggcaaggag atcttaatac ctaatttcat catttctgca aaatgtactg 3575
232 ttttagaatg tattacaata tcaatgtgaa tatcttgaat cctgttatac atcctgcact 3635
234 gtattaaaca tgtaaaattaa ttgtttgtct gattagccaa tctcaccacc caaatgggga 3695
236 ggtatacatg tttgaagaac gtgtaactcg gtaattgatt tgttctgatg ttgtaactca 3755
238 atagaagtgt tttggaagga agcatggtgt gtgagacagt gtctgttctt ttgtgccagc 3815
240 tctgtatgat gtttgaaga ccatgtttgt aagacatgaa taaattgctg cttttgccca 3875
242 aaaaaaaaaa aaaaaa 3891

```

245 &lt;210&gt; SEQ ID NO: 2

246 &lt;211&gt; LENGTH: 425

247 &lt;212&gt; TYPE: PRT

248 &lt;213&gt; ORGANISM: Homo sapiens

## &gt; 249 &lt;220&gt; FEATURE:

250 &lt;223&gt; OTHER INFORMATION: product = Repro-PC-1.0

252 &lt;400&gt; SEQUENCE: 2

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253 Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr
254 1 5 10 15
256 Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
257 20 25 30
259 Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
260 35 40 45
262 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
263 50 55 60
265 Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
266 65 70 75 80
268 Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
269 85 90 95
271 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
272 100 105 110
274 Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
275 115 120 125
277 Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
278 130 135 140
280 Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
281 145 150 155 160
283 Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
284 165 170 175
286 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
287 180 185 190
289 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
290 195 200 205
292 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr

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TIME: 16:00:51

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Output Set: N:\CRF4\12192003\I680121C.raw

```

293      210      215      220
295 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
296 225      230      235      240
298 Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
299      245      250      255
301 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
302      260      265      270
304 Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg
305      275      280      285
307 Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
308      290      295      300
310 Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
311 305      310      315      320
313 Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
314      325      330      335
316 Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
317      340      345      350
319 Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
320      355      360      365
322 Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
323      370      375      380
325 Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
326 385      390      395      400
328 Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile
329      405      410      415
331 Ala Lys Trp His Val Leu Cys Asp Gly
332      420      425

```

336 &lt;210&gt; SEQ ID NO: 3

337 &lt;211&gt; LENGTH: 21

338 &lt;212&gt; TYPE: DNA

339 &lt;213&gt; ORGANISM: Homo sapiens

341 &lt;220&gt; FEATURE:

342 &lt;221&gt; NAME/KEY: misc\_feature

343 &lt;222&gt; LOCATION: (1)..(21)

344 &lt;223&gt; OTHER INFORMATION: 5' oligo (109) Upper Primer

346 &lt;400&gt; SEQUENCE: 3

347 cagttttccc ttcagcacct c

21

350 &lt;210&gt; SEQ ID NO: 4

351 &lt;211&gt; LENGTH: 30

352 &lt;212&gt; TYPE: DNA

353 &lt;213&gt; ORGANISM: Homo sapiens

355 &lt;220&gt; FEATURE:

356 &lt;221&gt; NAME/KEY: misc\_feature

357 &lt;222&gt; LOCATION: (1)..(30)

358 &lt;223&gt; OTHER INFORMATION: 3' oligo (3489) Lower Primer

360 &lt;400&gt; SEQUENCE: 4

361 ttcctttgtt gtttcttttc tcttttctga

30

364 &lt;210&gt; SEQ ID NO: 5

365 &lt;211&gt; LENGTH: 425

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/680,121C

DATE: 12/19/2003  
TIME: 16:00:52

Input Set : A:\Amended Sequence Listing for 107-206-C-D.txt  
Output Set: N:\CRF4\12192003\I680121C.raw

ase Note:

of n and/or Xaa have been detected in the Sequence Listing. Please review the  
uence Listing to ensure that a corresponding explanation is presented in the <220>  
<223> fields of each sequence which presents at least one n or Xaa.

#:11; Xaa Pos. 1,2,3,4,5,6,7,8  
#:12; Xaa Pos. 1,2,3,4,5,6,7,8,9  
#:13; Xaa Pos. 1,2,3,4,5,6  
#:14; Xaa Pos. 1,2,3,4,5,6,7  
#:15; Xaa Pos. 1,2,3,4,5,6,7,8,9  
#:16; Xaa Pos. 1,2,3,4,5,6,7,8,9,10  
#:17; Xaa Pos. 1,2,3,4,5,6,7,8  
#:18; Xaa Pos. 1,2,3,4,5,6,7,8,9  
#:19; Xaa Pos. 1,2,3,4,5,6,7,8,9  
#:20; Xaa Pos. 1,2,3,4,5,6,7,8,9,10  
#:27; Xaa Pos. 5

## VERIFICATION SUMMARY

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Input Set : A:\Amended Sequence Listing for 107-206-C-D.txt

Output Set: N:\CRF4\12192003\I680121C.raw

49 M:283 W: Missing Blank Line separator, <220> field identifier  
46 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
55 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
64 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
83 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
92 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
01 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
10 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
20 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
49 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
58 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0  
77 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
86 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
96 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
05 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
14 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
24 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
43 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
52 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0  
71 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
80 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
89 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
08 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18  
17 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18  
26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18  
35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
54 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
63 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
72 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0  
91 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
000 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
009 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0  
121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27  
130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0